



COPY OF PAPERS
ORIGINALLY FILED

SEQUENCE LISTING

<110> Merck & Co., Inc.
University of British Columbia

<120> APOPTOSIS MODULATORS THAT INTERACT WITH
THE HUNTINGTON'S DISEASE GENE

RECEIVED

FEB 26 2002

TECH CENTER 1600/2900

<130> MC010PI

<140> 09/701,205

<141> 2000-11-27

<150> PCT/US99/11743

<151> 1999-05-27

<150> 09/085,199

<151> 1998-05-27

<160> 43

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1164

<212> DNA

<213> Human

<220>

<221> misc_feature

<222> (1)... (1164)

<223> n = A,T,C or G

<400> 1

acagctgaca	cctctgaagg	ccacggggac	cgcttcattg	agcagtttac	aaagtgtgaaa	60
gatctgttct	accgctccag	caacctgcag	tacttcaagc	gggtcattca	gatccccccag	120
ctgccttgaga	accaccccaa	cttctctgca	gcctcagccc	tgctcagaaca	tatcagccct	180
gtgggtgggtga	tcctctgcaga	ggcctcatcc	cccgacagcg	agccagtccct	agagaaggat	240
gacctcatgg	acatggatgc	ctcttcagcag	aatttatttg	acaacaagtt	tgatgaacttc	300
tttggcagtt	catccagcag	tgatcccttc	aatttcacaa	gtcaaaaatgg	tggtgaacag	360
gatgagaagg	accacttaat	tgagcgacta	tacagagaga	tcagtggatt	gaaggcacag	420
ctagaaaaca	tgaagactga	gagccagcgg	gttgtgtctg	agctgaaggg	ccacgtcagc	480
gagctgggaag	cagatctggc	cgagcagcag	cacctgcggc	agcaggcgcc	cgacgactgt	540
gaattctctgc	gggcagaaat	ggacgagctc	aggnngcgag	gggaggacac	cgagaaggct	600
cagcggagccc	tgtctgagat	agaaaaggaaa	gctcaagcca	atgaacagcg	atatagcaag	660
ctaaaaggaga	agtacagcga	gctgggttcag	aaccacgctg	acctgctcgc	gaagaatgca	720
gaggtgacca	aacaggtgtc	catggccaga	caagcccagg	tagatttggg	acgagagaaa	780
aaagagctgg	aggatctggt	ggagcgcctc	agtgaaccag	gcagcgggaa	gactcaaggaa	840
cagctgggaag	tcttagagag	cttgagcag	gaacttgga	caagcccaag	ggagcttcag	900
tctctgcagg	gcagcctgga	aacttctgcc	cagtcagaag	caactcagcc	agccgagttc	960
gccgagctag	agaaggagcg	ggacagcctg	gtgagtgagg	cagctcatag	ggaggaggaa	1020
ttatctgctc	tctggaaaaga	actgcaggac	actcagctca	aactggccag	cacagaggaa	1080
tctatgtgcc	agcttgccaa	agaccaacga	aaaatgcttc	tggtggggtc	caggaaggct	1140
cgaggacagg	tgatacaaga	cgcg				1164

<210> 2

<211> 386

<212> PRT

<213> Human

<400> 2

Thr Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe
 1 5 10 15
 Thr Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe
 20 25 30
 Lys Arg Val Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe
 35 40 45
 Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile
 50 55 60
 Pro Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp
 65 70 75 80
 Asp Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys
 85 90 95
 Phe Asp Asp Phe Gly Ser Ser Ser Ser Ser Asp Pro Phe Asn Phe Asn
 100 105 110
 Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
 115 120 125
 Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
 130 135 140
 Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
 145 150 155 160
 Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
 165 170 175
 Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Gln Arg
 180 185 190
 Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg Lys
 195 200 205
 Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr Ser
 210 215 220
 Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu Val
 225 230 235 240
 Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu Arg
 245 250 255
 Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln Gly
 260 265 270
 Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys Gln
 275 280 285
 Glu Leu Gly Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser Leu
 290 295 300
 Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala Glu
 305 310 315 320
 Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg Glu
 325 330 335
 Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu Lys
 340 345 350
 Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln Arg
 355 360 365
 Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile Gln
 370 375 380
 Asp
 385

<210> 3

<211> 4796

<212> DNA

<213> Human

<220>

<221> misc_feature

<222> (1)...(4796)

<223> n = A,T,C or G

<400> 3

caagtgtacgg	tgtgatcatat	aacgcccggg	ggggggattg	gtttatatat	cgcaaatgga	60
intagggggg	gggggatagg	caagagatttc	gottcattag	gccattataa	gcagggaagg	120
tttcaaggaa	aaaaaccaga	aaagtgcata	ttgacccac	catgagaaag	gggcaacaga	180
cettntgcttn	tgtntntcaac	cgctcgcttc	tgtttttagca	acgcagtggt	ttgggtggaag	240
ttgtgcgatg	ttgttccaaa	antcttcoga	gatggacacc	cgcaactctc	gaaggaccttt	300
gtgagatata	gaattgaatt	gagtgacatg	agcaggatgt	ggggccacct	gagcgagggg	360
tatggccagg	ttgttcagct	ctacctgaaa	ctgcagaaga	ccagatgaga	gtaccacacc	420
aaaaatccca	ggttccagg	caacctgcag	atgagtgaac	gccagctgga	cgaggctgga	480
gaaagtgcag	tgaacaacct	tttccagtta	acagttggaga	tgtttgacta	cctggagtggt	540
gaactcaacc	ttcttcaaac	agttatcca	tcctcggaca	tgctccgctc	tgtgtccgtg	600
acggcgagcag	ggcagctgcc	cctcgccccg	ctgatccagg	tcactcttga	ctcgacgccac	660
ctttatgact	acaactgtcaa	gcttctcttc	aaactccact	ctcgctctcc	agctgacacc	720
ctgcgaaggcc	acggggagcag	cttcatggag	cagtttacaa	agttgaaaga	tcgttctcac	780
cgctccagca	acctgcagta	cttcaaggcg	ctcatccaag	tcctccagct	cctgtgagaac	840
ccaccacaact	ctctgcgagc	ctcagccctg	tcagaaacata	tcagccctgt	ggctggtagc	900
cctgcagagc	ctctcatccc	cgacagcgag	ccagctctag	agaagaatga	ctctcatggac	960
atggatgctc	ctcagcagaa	tttatattgac	aaacaagttt	atgacatctt	tcgcagttca	1020
ttcagcagtg	atcccttcaa	tttcaacagt	caaaatggtg	tgaacaagga	tgagaaggac	1080
caactaaattg	agcgactata	caagagagatc	agtggattga	agggcacagt	agaaaacatg	1140
aagactggaga	gccagcgggt	tgtgctgcag	ctgaaggccc	acgtcagcga	gctggaaagca	1200
gactctgcgc	agcagcagca	cctgcggcag	caggcggccg	acgactgtga	atctctcgcg	1260
gcagaagctg	acagagctcag	gaggcagcgg	gaggacaccg	agaaggctca	gcggagcctg	1320
ttctgagctag	aaaggaaagc	taagaccgat	gaacacgcat	ataagcaagt	aaaggagaag	1380
tacagcagc	tgttctcaga	ccagctgcac	ctgtctgcga	agaaatcgaga	ggttgacaaa	1440
cagggtctcca	ggccagacaga	agcccaggta	gatttggaac	gagagaaaaa	agagagctgag	1500
gattcgttgg	agcgcataac	tgaccagggc	cagcggaaaga	ctcaagaaca	gctggaaagtt	1560
ctagagagct	tgaagcagga	acttggcaca	agccaacggg	agcttcaggt	ttctgcaaggc	1620
agcctggaaa	cttctgccca	gtcagaagca	aactggcgca	cggagtctgc	cgagctagag	1680
aaggagcggg	acagcctcgt	gagtgccgca	gctcataggg	aggaggaatt	atctgctctt	1740
cggaaagacc	tgacagcac	tcagctcaaa	ctggccagca	caggaggaatc	tatgtgccag	1800
cttgcocaaag	accaacgaaa	aatgctctct	gtgggggtcca	ggaaggctgc	ggagcaggtg	1860
atacaagacg	ccctgaacca	gcttgaagaa	cctcctctca	tcagctgcgc	tggtgtctgca	1920
gatcacctct	ttctccaggt	caactccatt	tcagctgcga	ctgagctaac	ggagaaaagc	1980
ttgagccagt	atctgcctct	cccagaagac	atcagtggaac	ttctccatc	cataacctct	2040
cttggccact	tgaccagcga	cgccattgct	catggtgcca	ccactcgctc	cagagcccca	2100
cttgcagctc	ccgactcaat	gaccgagccc	gttaagcagt	atggcaggga	aaacctcgcc	2160
taactggcct	cccttgaggga	agagggaagc	cttgagaatg	ccgcagcagc	agccatgag	2220
aaactgcctga	gcaagatcaa	ggccatcgcc	gaggagctcc	tgcccagggg	actggcacatc	2280
aagcagggagg	agctggggga	cctggtggac	aaggagatgg	cggccacttc	agctgctatt	2340
caactctgca	cgccaggaat	agaggagatg	ctcagcaaat	cccagcagag	agacacagga	2400
gtcaaatgga	gcttgactga	aagatcctt	cgttgtctga	ccagctccat	gcaagctatt	2460
gaggtgctca	ctctgctctc	taagaccctc	caagagagaa	ttgtggagag	cgccaggggt	2520
acagctatccc	ctaaagagtt	ttatgccaa	aactctcgat	ggacagaagg	acttatctca	2580
gcctccaaag	ctgtgggctg	gggagccact	gtcatgggtg	atgcagctga	tcctgtgtgta	2640
caaggcagag	ggaaatttga	ggagcttaat	gtgtgtcttc	atgaaattgc	tgctagatca	2700
gcccaagcttg	tggtcgatc	caadgtgaaa	gtatgaagg	acagccccaac	ctctagccag	2760
ctgcagcagg	ctctcctggg	agtgaaccag	gccactgcgc	gcgttgtggc	ctcaaccatt	2820
tcgcgcaaat	cacagatcga	agadacagac	aaactaggact	tctcaagcat	gacgtcgaca	2880
cagatcaaac	gccaaagatg	ggatctccag	gttaggggtc	tagagctaga	aaagctatga	2940
cagaagggagc	gtcaaaaact	gggagagctt	cggaataagc	actacagact	ctgtggtgtt	3000
gctgagggct	gggaagaagg	aacagagcca	tctccacctc	caactgcaag	agtgttaaac	3060
gaaaaagaat	agagccaaac	caacaccoca	tatgtcagtg	taactctctg	ttacttatct	3120
cggtgtgtgtt	atttcccagc	ccacaggcca	aactcctgga	gtcccagggg	cagccacac	3180
actgcacatta	cccagctgcc	aggacatgca	tgacactttc	caaaagatccc	tcgatagcga	3240
caccctttct	gtttggacc	atggtcatct	ctgtttttct	cccgctctcc	tcttgatgat	3300
ccagctcggc	cagtgctgcc	catgagcaag	ctaggtacag	aaagggggtg	gtgggggggca	3360
ggggcaactca	gcagcagga	ccaacatcca	gtcctctgta	ctatctgacc	cccaacaaca	3420
tggttatcct	taaaacagga	gctacttgt	gtttgttgac	agcttggaag	gggaagatct	3480
tatgctcttt	ctttcttgtt	tcttctcag	tcttttcagt	ttcatcatt	gtcaaaactt	3540
gtgacgtgca	gaggctgat	ggattccaaa	ccaggacact	accctgagat	ccacagctc	3600
agaaggacgg	caggagtgtc	ctggctgtga	atgccaaagc	cattctctccc	ctcttggggc	3660

```

agtgccatgg atttccactg cttcttatgg tggttgggtg gggttttttg tttgtttttt 3720
tttttttaag ttttactcac atagccaact ctcaccaagg gcacacccct ggggctgagt 3780
ctccaggggc ccccaactgt ggtagctcca gcgatgggtc tgcccaggcc tctcggtgct 3840
ccatctccgc ctccacactg accaagtgtc ggcccaccca gtccatgtct cagggtcagg 3900
cggagactgt gagtgcacgc tttctcaaaa aagcagaagg agagttagtg cctttccctc 3960
ctaaagctcg atccagctcg aaagcctctg tccgccttta caaggagaga gacaacagaa 4020
agagggacaa gaggggtcac acagcccgag tccgtgagc aggtcaaaa actgatcac 4080
atgcttgaat gagctgggtg agatcaacaa cactacttcc ctgcccgaat gaactgtccg 4140
tgaattgtct ctgtcaaggc ggccgtctcc cttggcccag agacggagtg tgggagtgat 4200
tcccactccc tttctgcaga cgtctgcctt ggcatctctt tgaataggaa gatcgttcca 4260
ctttctacgc aattgacaaa cccggaagat cagatgcaat tgctcccatc agggagaaga 4320
cctatacttg gtttgcacc cttagtattt attactaacc tcccttaagc agcaacagcc 4380
tacaaagaga tgcttggagc aatcagaact tcaggtgtga ctctagcaaa gctcatcttt 4440
ctgcccggct acatcagcct tcaagaatca gaagaaagcc aaggtgctgg actgttactg 4500
acttggatcc caaagcaagg agatcatttg gagctcttgg gtcagagaaa atgagaaagg 4560
acagagccag cggtctccac tctcttcagc cacatgcgcc agctctcgc tgccctgtgg 4620
acagagatag gacagagggc acatgaacag cttgccaggg atgggcagcc caacagcact 4680
tttctcttct tagatggacc ccagcattta agtgaccttc tgatcttggg aaaaacagct 4740
cttctcttct tatctatagc aactcatttg tggtagccat caagcacttc ggaatt 4796

```

```

<210> 4
<211> 914
<212> PRT
<213> Human

```

A1

```

<400> 4
Met Ser Arg Met Trp Gly His Leu Ser Glu Gly Tyr Gly Gln Leu Cys
1 5 10 15
Ser Ile Tyr Leu Lys Leu Leu Arg Thr Lys Met Glu Tyr His Thr Lys
20 25 30
Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
35 40 45
Glu Ala Gly Glu Ser Asp Val Asn Phe Phe Gln Leu Thr Val Glu
50 55 60
Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
65 70 75 80
Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
85 90 95
Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu
100 105 110
Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
115 120 125
Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe Thr
130 135 140
Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys
145 150 155 160
Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu
165 170 175
Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro
180 185 190
Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp
195 200 205
Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe
210 215 220
Asp Asp Ile Phe Gly Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn
225 230 235 240
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
245 250 255
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
260 265 270
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
275 280 285

```

Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
 290 295 300
 Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg Gln
 305 310 315 320
 Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg
 325 330 335
 Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr
 340 345 350
 Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu
 355 360 365
 Val Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu
 370 375 380
 Arg Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln
 385 390 395 400
 Gly Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys
 405 415
 Gln Glu Leu Gly Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser
 420 425 430
 Leu Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala
 435 440 445
 Glu Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg
 450 455 460
 Glu Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu
 465 470 475 480
 Lys Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln
 485 490 495
 Arg Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile
 500 505 510
 Gln Asp Ala Leu Asn Gln Leu Glu Glu Pro Pro Leu Ile Ser Cys Ala
 515 520 525
 Gly Ser Ala Asp His Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys
 530 535 540
 Ile Glu Gln Leu Glu Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu
 545 550 555 560
 Asp Ile Ser Gly Leu Leu His Ser Ile Thr Leu Leu Ala His Leu Thr
 565 570 575
 Ser Asp Ala Ile Ala His Gly Ala Thr Thr Cys Leu Arg Ala Pro Pro
 580 585 590
 Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Lys Gln Tyr Gly Arg Glu
 595 600 605
 Thr Leu Ala Tyr Leu Ala Ser Leu Glu Glu Glu Gly Ser Leu Glu Asn
 610 615 620
 Ala Asp Ser Thr Ala Met Arg Asn Cys Leu Ser Lys Ile Lys Ala Ile
 625 630 635 640
 Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu Glu Leu
 645 650 655
 Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu
 660 665 670
 Thr Cys Thr Ala Arg Ile Glu Glu Met Leu Ser Lys Ser Arg Ala Gly
 675 680 685
 Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Arg Cys Cys
 690 695 700
 Thr Ser Leu Met Gln Ala Ile Gln Val Leu Ile Val Ala Ser Lys Asp
 705 710 715 720
 Leu Gln Arg Glu Ile Val Glu Ser Gly Arg Gly Thr Ala Ser Pro Lys
 725 730 735
 Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala
 740 745 750
 Ser Lys Ala Val Gly Trp Gly Ala Thr Val Met Val Asp Ala Ala Asp
 755 760 765
 Leu Val Val Gln Gly Arg Gly Lys Phe Glu Glu Leu Met Val Cys Ser
 770 775 780

His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val
 785 790 795 800
 Lys Ala Asp Lys Asp Ser Pro Asn Leu Ala Gln Leu Gln Ala Ser
 805 810 815
 Arg Gly Val Asn Gln Ala Thr Ala Gly Val Val Ala Ser Thr Ile Ser
 820 825 830
 Gly Lys Ser Gln Ile Glu Glu Thr Asp Asn Met Asp Phe Ser Ser Met
 835 840 845
 Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val Arg Val
 850 855 860
 Leu Glu Leu Glu Asn Glu Leu Gln Lys Glu Arg Gln Lys Leu Gly Glu
 865 870 875 880
 Leu Arg Lys Lys His Tyr Glu Leu Ala Gly Val Ala Glu Gly Trp Glu
 885 890 895
 Glu Gly Thr Glu Ala Ser Pro Pro Thr Leu Gln Glu Val Val Thr Glu
 900 905 910
 Lys Glu

<210> 5
 <211> 1090
 <212> PRT
 <213> Human

<400> 5
 Met Leu Leu Cys Gln Gly Ser Glu Trp Arg Arg Asp Gln Gln Leu Gly
 1 5 10 15
 Thr Ala Asn Ala Arg Gln Trp Cys Pro Leu Pro Gln Asp Ala Gln Pro
 20 25 30
 Ala Gly Ser Trp Glu Arg Cys Pro Pro Leu Pro Pro Ala Gly Arg Leu
 35 40 45
 Gln Gly Thr Asp His Pro Trp Gly Trp Gly Arg Leu Ala Gly Gly Gly
 50 55 60
 Glu Arg Gly Gly Leu Trp Glu Gly Leu Ser His Ser Gln Arg Leu Ile
 65 70 75 80
 His Leu Ile Leu Leu Ser Leu Pro Leu Leu Val Phe Gln Thr Val Ser
 85 90 95
 Ile Asn Lys Ala Ile Asn Thr Gln Glu Val Ala Val Lys Glu Lys His
 100 105 110
 Ala Arg Thr Cys Ile Leu Gly Thr His His Glu Lys Gly Ala Gln Thr
 115 120 125
 Phe Trp Ser Val Val Asn Arg Leu Pro Leu Ser Ser Asn Ala Val Leu
 130 135 140
 Cys Trp Lys Phe Cys His Val Phe His Lys Leu Leu Arg Asp Gly His
 145 150 155 160
 Pro Asn Val Leu Lys Asp Ser Leu Arg Tyr Arg Asn Glu Leu Ser Asp
 165 170 175
 Met Ser Arg Met Trp Gly His Leu Ser Glu Gly Tyr Gly Gln Leu Cys
 180 185 190
 Ser Ile Tyr Leu Lys Leu Leu Arg Thr Lys Met Glu Tyr His Thr Lys
 195 200 205
 Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
 210 215 220
 Glu Ala Gly Glu Ser Asp Val Asn Asn Phe Phe Gln Leu Thr Val Glu
 225 230 235 240
 Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
 245 250 255
 Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
 260 265 270
 Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu
 275 280 285
 Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro

290
 Ala Asp Thr Leu Gln Gly 295
 305 Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser 315 Phe Met Glu Gln Phe Thr 320
 Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu 335
 Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro 345
 Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp 350
 Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe 365
 385 Asp Asp Ile Phe Gly Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn 395
 Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg 410
 Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys 425
 Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu 440
 Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala 455
 465 Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg 475
 Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg 485
 Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr 495
 Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu 510
 Val Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu 525
 Arg Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln 540
 Gly Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys 555
 Gln Glu Leu Ala Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser 570
 Leu Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala 585
 Glu Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg 600
 625 Glu Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu 615
 Lys Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln 630
 Arg Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile 645
 Gln Asp Ala Leu Asn Gln Leu Glu Pro Pro Leu Ile Ser Cys Ala 660
 Gly Ser Ala Asp His Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys 675
 705 Ile Glu Gln Leu Glu Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu 690
 Asp Ile Ser Gly Leu Leu His Ser Ile Thr Leu Leu Ala His Leu Thr 715
 Ser Asp Ala Ile Ala His Gly Ala Thr Thr Cys Leu Arg Ala Pro Pro 730
 Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Lys Gln Tyr Gly Arg Glu 745
 Thr Leu Ala Tyr Leu Ala Ser Leu Glu Glu Glu Gly Ser Leu Glu Asn 760

A

A

A

ggctcccacc gacctcgccg accgectcat agacacctgc agggagtagcg gggcccgggc 1020
 tctggagctc atggggcagc gcaggctctg cggcacatgc agccagcctt 1080
 ggtgcggaca cccctcgagg gcatccttca gctgggccaag gactgaagac ccaagagcctt 1140
 agatgtcgcg caggagagc tgggggcccgt ggtcgacaag gagatggcg ccacatccgc 1200
 atcgatgtgaa gatgtctgtgc ggaggatgga ggacatgatg aaccaggcac gccacggcag 1260
 ctgggggtgc aagctggagg tgaacgagag gatcctcaac tctgcacag accctgatgaa 1320
 ggctatccgg ctctcgttga cgacatccac tagcctgcag aaggagatcg tggagagcgg 1380
 caggggggga gccacgcagc aggaatttta cgccaagaac tcgcgctgga cgcgaaggcct 1440
 catctcgcc cccaaggctg tgggtcgggg agccaacag ctggtggagc cagctgaca 1500
 ggtgtgctt cacaacggca agtatgagga gctcatcgtc tgctccacg agatcgagc 1560
 cagcacggcc cagctggtgg cgcctccaa ggtgaaggcc aacaagcaca gcccccact 1620
 gagccgctgt caggaatgtt ctgcacagc caatgagagg gctgcgaatg tgggtggcct 1680
 caccagtca gggcaggagc agattgagga cagagacacc atgatttct ccgctctgtc 1740
 cctcatcaag ctgaagaagc agggagatgga gacgcagggt cgtgtcctgt agctggagaa 1800
 gacgtggag gctgaacgca tgcggctggg ggagttgccc aagcaacact acgtgctggc 1860
 tggggcatca ggcagccctg gagaggaggt gggcatccgg ccacgactgt ccccccgaag 1920
 tgaacaacc aagaacacc ccttggccca agcccagc gtggcccca gacagggaca 1980
 ccagcttgac aaaaggatg gcatcacc agctcaactc gtgaactact aggccecca 2040
 ggggtccagc aggggtggct gtgacagccc tgggctctgt caactgccct gacaggaccg 2100
 agaggcctgt cccctccacc tgggtcccaa gcctcccgc ccacgctgt gatcaatgtc 2160
 ctaaggagcc ctggccctta ctgagcctgc agggctcctg gccatgtggg tgggtgctct 2220
 ggaatgagct ctctatttta tctgcagaag gaactttggg gtgcagccag gaccggtag 2280
 gctcgagcct caactcttca gaaaatagtg ttttataat tctcttcag aaaaatagtg 2340
 ttttaattat gctctctaga gctctcttca ctacgtttgt agtcagatg atgggaaacc 2400
 gggccagcgt ggggctcctt gctctctgga ctctggaag ctgtgagtg atggaaagca 2460
 caccgcccgt gcgcgtgat gcagcagagg tcaggcatc tgctgtgggc ctctggggc 2520
 accgattcta ccaggccctc cagctcgtg gtctccgac accaggctct gttctgggcta 2580
 gaggaaatgt gcccatacc tctcagggc ctggccctcg ggctcctgt atggagccc 2640
 cccaggaggg tccagatgtc ggaaggggcc gctttctggg gagtgaagtg agacatagcg 2700
 gccagggcgc tgctttcact cctggaagtt ccatcttccg ctggaaatct cagccacccc 2760
 catttctgt tttctattcc cccgttctgg ccgcgcccga ctgcccact gaagggtgg 2820
 tttccagccc tccggagagt gggcttggcc ctaggccctc cagctcagcc agaaaaagcc 2880
 cagaaaaacca ggtctgggac caggccctc agggaggagc cctgcggcta gagtgggcta 2940
 ggccctggct ttgcgcgtca gatttgaac aatgtgtc ccttgagccc aaggaaggg 3000
 gcaggaggcg tgggacagg ctgggaggac agagccagca gctgccatgc cctctgctc 3060
 ccccacccc agcctagccc ctttagcctt tcacctgtg ctctggaagc gtataccaat 3120
 actggccaag gtgaggagga gcaaaaaatg gccagcaca gcgccttggc tttgtgtag 3180
 catttctccc tgaagtgttc gtttggcaat aaatgcact ttgactgtta aaaaaaaa 3240
 aaaaaaaa a 3251

<210> 7
 <211> 676
 <212> PRT
 <213> Human

<400> 7
 Gly Glu Leu Glu Glu Gln Arg Lys Gln Lys Gln Lys Ala Leu Val Asp
 1 5 10 15
 Asn Glu Gln Leu Arg His Glu Leu Ala Gln Leu Arg Ala Ala Gln Leu
 20 25 30
 Glu Arg Glu Arg Ser Gln Gly Leu Arg Glu Glu Ala Glu Arg Lys Ala
 35 40 45
 Ser Ala Thr Glu Ala Arg Tyr Asn Lys Leu Lys Glu Lys His Ser Glu
 50 55 60
 Leu Val His Val His Ala Glu Leu Leu Arg Lys Asn Ala Asp Thr Ala
 65 70 75 80
 Lys Gln Leu Thr Val Thr Gln Gln Ser Gln Glu Glu Val Ala Arg Val
 85 90 95
 Lys Glu Gln Leu Ala Phe Gln Val Glu Gln Val Lys Arg Glu Ser Glu
 100 105 110
 Leu Lys Leu Glu Glu Lys Ser Asp Gln Gln Glu Lys Leu Lys Arg Glu
 115 120 125

Leu Glu Ala Lys Ala Gly Glu Leu Ala Arg Ala Gln Glu Ala Leu Ser
 130 135 140
 His Thr Glu Gln Ser Lys Ser Glu Leu Ser Ser Arg Leu Asp Thr Leu
 145 150 155 160
 Ser Ala Glu Lys Asp Ala Leu Ser Gly Ala Val Arg Gln Arg Glu Ala
 165 170 175
 Asp Leu Leu Ala Ala Gln Ser Leu Val Arg Glu Thr Glu Ala Ala Leu
 180 185 190
 Ser Arg Glu Gln Gln Arg Ser Ser Gln Glu Gln Gly Leu Gln Gly
 195 200 205
 Arg Leu Ala Glu Arg Glu Ser Gln Glu Gln Gly Leu Arg Gln Arg Leu
 210 215 220
 Leu Asp Glu Gln Phe Ala Val Leu Arg Gly Ala Ala Glu Ala Ala
 225 230 235 240
 Gly Ile Leu Gln Asp Ala Val Ser Lys Leu Asp Asp Pro Leu His Leu
 245 250 255
 Arg Cys Thr Ser Ser Pro Asp Tyr Leu Val Ser Arg Ala Gln Glu Ala
 260 265 270
 Leu Asp Ala Val Ser Thr Leu Glu Glu Gly His Ala Gln Tyr Leu Thr
 275 280 285
 Ser Leu Ala Asp Ala Ser Ala Leu Val Ala Ala Leu Thr Arg Phe Ser
 290 295 300
 His Leu Ala Ala Asp Thr Ile Ile Asn Gly Gly Ala Thr Ser His Leu
 305 310 315 320
 Ala Pro Thr Asp Pro Ala Asp Arg Leu Ile Asp Thr Cys Arg Glu Cys
 325 330 335
 Gly Ala Arg Ala Leu Glu Leu Met Gly Gln Leu Gln Asp Gln Gln Ala
 340 345 350
 Leu Arg His Met Gln Ala Ser Leu Val Arg Thr Pro Leu Gln Gly Ile
 355 360 365
 Leu Gln Leu Gly Gln Glu Leu Lys Pro Lys Ser Leu Asp Val Arg Gln
 370 375 380
 Glu Glu Leu Gly Ala Val Asp Lys Glu Met Ala Ala Thr Ser Ala
 385 390 395 400
 Ala Ile Glu Asp Ala Val Arg Arg Ile Glu Asp Met Met Asn Gln Ala
 405 410 415
 Arg His Ala Ser Ser Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu
 420 425 430
 Asn Ser Cys Thr Asp Leu Met Lys Ala Ile Arg Leu Leu Val Thr Thr
 435 440 445
 Ser Thr Ser Leu Gln Lys Glu Ile Val Glu Ser Gly Arg Gly Ala Ala
 450 455 460
 Thr Gln Gln Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu
 465 470 475 480
 Ile Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Gln Leu Val Glu
 485 490 495
 Ala Ala Asp Lys Val Val Leu His Thr Gly Lys Tyr Glu Glu Leu Ile
 500 505 510
 Val Cys Ser His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala
 515 520 525
 Ser Lys Val Lys Ala Asn Lys His Ser Pro His Leu Ser Arg Leu Gln
 530 535 540
 Glu Cys Ser Arg Thr Val Asn Glu Arg Ala Ala Asn Val Val Ala Ser
 545 550 555 560
 Thr Lys Ser Gly Gln Glu Gln Ile Glu Asp Arg Asp Thr Met Asp Phe
 565 570 575
 Ser Gly Leu Ser Leu Ile Lys Leu Lys Lys Gln Glu Met Glu Thr Gln
 580 585 590
 Val Arg Val Leu Glu Leu Glu Lys Thr Leu Glu Ala Glu Arg Met Arg
 595 600 605
 Leu Gly Glu Leu Arg Lys Gln His Tyr Val Leu Ala Gly Ala Ser Gly
 610 615 620

Ser Pro Gly Glu Glu Val Ala Ile Arg Pro Ser Thr Ala Pro Arg Ser
 625 630 635 640
 Val Thr Thr Lys Lys Pro Pro Leu Ala Glh Lys Pro Ser Val Ala Pro
 645 650 655
 Arg Glh Asp His Glh Leu Asp Lys Lys Asp Gly Ile Tyr Pro Ala Glh
 660 665 670
 Leu Val Asn Tyr
 675

<210> 8
 <211> 2301
 <212> DNA
 <213> Mouse

<400> 8
 ggccagaggg ctcattcaga tccccagct gcccgagaat ccaccaact tctacgagc 60
 ctggccctct tcagagccaca tcagctctgt ggtggatgc ccggcagagg tctatcccc 120
 agacagctgag cctgtccctgg agaaggatga cctcatggac atggacgcct cccagcagac 180
 ttgttttgag acaaatgttg atgacgtctt tggcagctca ttgagcagcg accctttcaa 240
 ttccaacaat caaaatggcg tgaacaagga cgagaaggac cacttgattg aacgcctgtg 300
 cagagagatc agtggaactga cagggcagct ggacaacatg aagattgaga gccagcggcg 360
 catgctcgag ctgaagggtc gagtgcagtga gctggaggca gagctagcag agcagcagca 420
 ctgggcccgg caggctagct atgactgcga gttcctgcgc actgagctgg atgaactgaa 480
 gagggcagcga gaggacacgg agaaggcaca gcgcagcctg actgagatag aaagaaggagc 540
 ccaggctaat gaacagaggt atagcaagtt aaaaagagaac tacagtgaa cgtgtcgaga 600
 ccagtctgag ctgctcgaga agaaccgaga ggtgacaaa caggtgtccg tggcccgcca 660
 agcccaagtg gatttgaaaa gagagaaaaa agagctagca gattcctttg cactgttaag 720
 tgaccagccc cagcgggaaga ctcaagagca acagagtggt ctagaagaac tgaagcatga 780
 actggccacc agcagaacag agctgcaggt cctccacgc cactggaaa cctctgccca 840
 gtcagaagcg aaatggctga cacagatcgc cgagttggag aaggacaacg gcagcttggc 900
 gactgttgca gctcagagag aggaagagtt atcacgcttc cgagaccagc tggaaagcac 960
 ccagatacag ctggctggggg cccaggaatc catgtgccag caggtgaagg accagagaaa 1020
 aacctctctg caggggatca ggaaggctgc ggagcgtgag atacaggagg cgctgagcca 1080
 gcttgaggaa cccaccctca tcagctgtgc aggatccaca gatcaccttc tctccaaagt 1140
 cagctccggt tccagctgcc tcgagcaact ggaaaaaagc ggcagccagt atctggcctg 1200
 cccagaagat attagtgagc ttctgcactc gatcacctct cttgccactt cagccgtga 1260
 cactgtcacc caggggagtg ccaccagcct ccgggcccga ccggagccag cegactcgtt 1320
 gacggagccc tgtaggcagt atggcagaga aacctggccc tatctgtcct ccttgaggga 1380
 agagggaact gtggagaatg ctgacgtcac agcccttagg aattgcctca gcaggggtcaa 1440
 gaccttggc gaggagctgc tgcccagggg cctggacatc aagcaggaag agctgggtga 1500
 cctggtggac aaggagatgg cagccacttc agctgccatt gaagctgccca ccaccgggat 1560
 agagaagaat ctcaatgaat ccagcaggg agacagcggg ctcaagctgg agtgaaatga 1620
 gaggatccg ggttccgtga ccagcctgat gcaggccata aagtgctcg ttgtgcctc 1680
 caaggacctc cagaaggaga tagtgagag tgccaggggt agtgcattcc ctaaagaatt 1740
 ttaagccaa aactctcggt ggacgggaag gctgatattc gctccaaaag ctgttggttg 1800
 gggagctacc atctgtgtgg atgtctgtga tctgtgtgct caaggcaaa ggaagtctga 1860
 ggagctgatg ttgtgttcac gcgagattgc tgccagtct gccagctct gctgtgcatc 1920
 caagtgtaaa gcgaacaagg gcagcctcaa tctgacccag ctgcagcagg cctctcgagg 1980
 agtgaaccag gccacagccg ctgtgtgtgc ctcaaccatt tctggcaaat ctgagattga 2040
 ggaacaagac agtatggact tctcaagcat gacactgacc cagatcaagc gccagagatg 2100
 ggaatccag gttatgtgag ttgagctgga aatgcactg cagaagagc gtcagaaagt 2160
 aggaagacta cggaagaaac actacagact ggaaggcgta gctgagggct gctgaggaag 2220
 cagacaagca tcacgtctta ctgtccaaga agcaataacc gacaaaagat agagccaagc 2280
 cgacacccca cacatcagaa a

<210> 9
 <211> 756
 <212> PRT
 <213> Mouse

<400> 9
 Ala Arg Gly Leu Ile Glh Ile Pro Glh Leu Pro Glu Asn Pro Pro Asn

1 5 10 15
 Phe Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val
 20 25 30
 Ile Pro Ala Glu Val Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys
 35 40 45
 Asp Asp Leu Met Asp Met Asp Ala Ser Gln Gln Thr Leu Phe Asp Asn
 50 55 60
 Lys Phe Asp Asp Val Phe Gly Ser Ser Leu Ser Ser Asp Pro Phe Asn
 65 70 75
 Phe Asn Asn Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile
 85 90 95
 Glu Arg Leu Tyr Arg Glu Ile Ser Gly Leu Thr Gly Gln Leu Asp Asn
 100 105 110
 Met Lys Ile Glu Ser Gln Arg Ala Met Leu Gln Leu Lys Gly Arg Val
 115 120 125
 Ser Glu Leu Glu Ala Glu Leu Ala Glu Gln Gln His Leu Gly Arg Gln
 130 135 140
 Ala Met Asp Asp Cys Glu Phe Leu Arg Thr Glu Leu Asp Glu Leu Lys
 145 150 155
 Arg Gln Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Thr Glu Ile
 160 165 170
 Glu Arg Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu
 175 180 185
 Lys Tyr Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn
 190 195 200
 Ala Glu Val Thr Lys Gln Val Ser Val Ala Arg Gln Ala Gln Val Asp
 205 210 215
 Leu Glu Arg Glu Lys Lys Glu Leu Ala Asp Ser Phe Ala Arg Val Ser
 220 225 230
 Asp Gln Ala Gln Arg Lys Thr Gln Glu Gln Gln Asp Val Leu Glu Asn
 235 240 245
 Leu Lys His Glu Leu Ala Thr Ser Arg Gln Glu Leu Gln Val Leu His
 250 255 260
 Ser Asn Leu Glu Thr Ser Ala Gln Ser Glu Ala Lys Trp Leu Thr Gln
 265 270 275
 Ile Ala Glu Leu Glu Lys Glu Gln Gly Ser Leu Ala Thr Val Ala Ala
 280 285 290
 Gln Arg Glu Glu Glu Leu Ser Ala Leu Arg Asp Gln Leu Glu Ser Thr
 295 300 305
 Gln Ile Lys Leu Ala Gly Ala Gln Glu Ser Met Cys Gln Gln Val Lys
 310 315 320
 Asp Gln Arg Lys Thr Leu Leu Ala Gly Ile Arg Lys Ala Ala Glu Arg
 325 330 335
 Glu Ile Gln Glu Ala Leu Ser Gln Leu Glu Glu Pro Thr Leu Ile Ser
 340 345 350
 Cys Ala Gly Ser Thr Asp His Leu Leu Ser Lys Val Ser Ser Val Ser
 355 360 365
 Ser Cys Leu Glu Gln Leu Glu Lys Asn Gly Ser Gln Tyr Leu Ala Cys
 370 375 380
 Pro Glu Asp Ile Ser Glu Leu Leu His Ser Ile Thr Leu Leu Ala His
 385 390 395
 Leu Thr Gly Asp Thr Val Ile Gln Gly Ser Ala Thr Ser Leu Arg Ala
 400 405 410
 Pro Pro Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Arg Gln Tyr Gly
 415 420 425
 Arg Glu Thr Leu Ala Tyr Leu Ser Ser Leu Glu Glu Glu Gly Thr Val
 430 435 440
 Glu Asn Ala Asp Val Thr Ala Leu Arg Asn Cys Leu Ser Arg Val Lys
 445 450 455
 Thr Leu Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu
 460 465 470
 Glu Leu Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala
 475 480 485 490 495

Ile Glu Ala 500
 515
 Ala Gly Asp Thr Thr Arg 505
 520
 Ser Cys Thr Ser Leu Met 535
 540
 Lys Asp Leu Gln Lys Glu Ile Val 545
 550
 Pro Lys Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile 570
 580
 Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Ile Met Val Asp Ala 595
 600
 Ala Asp Leu Val Val Gln Gly Lys Gly Lys Phe Glu Glu Leu Met Val 610
 615
 Cys Ser Arg Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser 625
 630
 Lys Val Lys Ala Asn Lys Gly Ser Leu Asn Leu Thr Gln Leu Gln Gln 645
 650
 Ala Ser Arg Gly Val Asn Gln Ala Thr Ala Ala Val Val Ala Ser Thr 660
 665
 Ile Ser Gly Lys Ser Gln Ile Glu Glu Thr Asp Ser Met Asp Phe Ser 670
 675
 Ser Met Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val 685
 690
 Arg Val Leu Glu Leu Glu Asn Asp Leu Gln Lys Glu Arg Gln Lys Leu 700
 705
 Gly Glu Leu Arg Lys Lys His Tyr Glu Leu Glu Gly Val Ala Glu Gly 710
 715
 Trp Glu Glu Gly Thr Glu Ala Ser Pro Ser Thr Val Gln Glu Ala Ile 720
 725
 Pro Asp Lys Glu 735
 740
 745
 750
 755

<210> 10
 <211> 3979
 <212> DNA
 <213> Mouse

<400> 10
 ggcacgaggc ggcgcgcggc ctcctgtgtc ctaggcttga ggcggggcgt gacgcctcat 60
 tgcgcggagc cgggcccggg acacggtcgg cggcagcatg aacagcatca agaastgtgcc 120
 ggcgcgggtg ctgagccgca ggcgcggcca cagctagag gccagtcgc agcagttcga 180
 caagacgcag gccatcagta tcagcaaaagc catcaacagc caggaggccc cagtgaaaga 240
 gaagcatgcc cggcgtatca tctctggcac gcatcatgag aaggaggcct tcactctctg 300
 gtctcttgcc atcgccctgc cgctgtccag cagctccatc ctcagctgga agttctgtca 360
 cgtctctcac aaggtctctc gggacggaca ccccaacgtc ctgcatgact atcagcggtta 420
 cggagacaac atacgtgaga tcgggtgact gtggggccac cttcgtgacc agtatggaca 480
 cctgggtgaat atctatacca aactgttgct gactaagatc tctctccacc ttaagcaccc 540
 Ccagttctct gcagccctcgg aggtaaacaga tgaggtgttg gagaaggcgg cgggaaactga 600
 tgtcaaacac atttttcagc ttacgctgga gatlgttgac taatggact gtgaactgaa 660
 gctttctgag tcaagtttct ggcagctcaa cagcgccatc gcaagtgccc agatgtctc 720
 tggccagtggt cgcttagcgc cgctcatcca ggtcattcag gactgcagcc acctgtacca 780
 ctacacagtg aagctcatgt ttaagctgca ctctgtctc ceggcagaca ccttgcaagg 840
 ccacagggat cggttccacg agcagttcca cagctccaaa aactctctcc gcggggcttc 900
 agacatcgtg tacttcaaga ggctcatcca gatcccgagg gaccccccaa 960
 ttctctcggt gcttcagccc tggctgagca catcaagccg gtgggtgtga ttcccaggga 1020
 ggcgccagag gaagaggagc ctgagaacct aattgaaatc agcagtgccg cctctgctgg 1080
 ggagccagtg gtggtgctg acctcttga tcagacacct ggacccccca atggctctcat 1140
 gaagatgac agggacctcc aatcgagaa ctggaagaca gaggtgagga cctcctgtgc 1200
 tgcagtgagc aagattaaga tggaggcaca gcgtacatc tcccaactga agggcaggt 1260
 gaatggcctg gaggcagagc tggaggagca gcgcaagcag aagcagaagg ccttggttga 1320

caacgagcag ctgcgccacg agctggccca gctcaaggcc ctgcagctgg agggcgcccg 1380
 caaccaggcc cttcgagagg aagcagagag gaaggccagt gccacggagg caccgtacag 1440
 caagctgaag gagaacaaca gcgaactcat taacacgcac gccagctgc tcaggaaagaa 1500
 cgacagacag ccgaacgagc tgacagtgaac acagcagagc caggaggagg tggccagcgg 1560
 aaaggaaacag ctggccttcc agatggagca agcgaagcgt gagtctgaga tgaagtatga 1620
 agagcagagc gaccagttgg aagaagctcaa gaggagctg gcggccaggg caggagagct 1680
 ggcctgctgg caggaggccc tgagccgcac agaacagagt gggctcagagc tgagctcacg 1740
 gctggacaca agctccggg agaaggagc cctgagctga gctgtctggc agctggagc 1800
 agactgctg ctgcgtcaga gctcgtgctg gaggagagg gaggcgctta gccaaagaga 1860
 cgacgcgagg tcccaggaga agggcgagct accggggcag ctggcagaaa aggagtctca 1920
 ggagcagagg ctctggcaga agctcgttga tgagcagtgg gcggtgttgc gaagtgcagc 1980
 cgccagggca gaggccatcc tacaggatgc agtgagcaag ctggacgacc cccctgcacct 2040
 ccgctgcacc agctcccccag actacttggt gaggccggct caggcagccc tggacagcgt 2100
 gaggcgctg gaggcaggcc acacccagta cctggcttcc tcggaagatg cttctgcctt 2160
 ggtggcagcg ctgaccgcct tctccattt ggtgcggac accattgtca attggtgccg 2220
 caccctccac ctggccccc cgcaccgcgc cgaccgcctg atggacacat gcaggaggtg 2280
 tgagccccc gctctggagc tggctgggaca gctgcaagc cagacagtgc taaggaggc 2340
 tcagcccaag ctgagtcggg ccccccctgca gggcattctc cagttggggc aggacttgaa 2400
 gccaaagac ctgagtgatc ggcaagagga gctaggggcc atggtggaca aggagatggc 2460
 ggccaccctc gctcgcagtg aggacgtgt gcggaggatc gaggacatga tgagccaggc 2520
 ccgcccagag agctcaggcg tgaacttggg ggtgaatgag aggatctcta actcctgcac 2580
 agactgatg aaggctatcc ggctcctggt gatgacctcc accagcctgc agaaggaaat 2640
 tgtggagagc ggcagggggg cagcaacgca cgaggaaatt tatgccaa gaattcaggtg 2700
 gactgaagcc ctactctcag cctctaaagg agtgggctgg ggagccacac agctggttga 2760
 ctcaagtac aggtttgctg ttcacatggg caaatcagag gaactcatgc tctgtccca 2820
 tgagattggc gccagcacgg cccagctggt ggcagctctg aaggtgaaag ccacaagaaa 2880
 cagctcccac ttgagccgcc tgcaggaatg ttcccgcact gtcaacgaga gggctgccaa 2940
 cgtctgtggc tccacaaatc ctggccagga gcagattgag gacagagaca ccatggattt 3000
 cctcggctg tcccctatca agttgaagaa gcaggagatg gagacacagg tgcagattct 3060
 ggagctggag aagacactag aggcagagcg tgtccggctc ggggagcttc ggaacacaga 3120
 ctatgtactg cctggggggga tgggaacacc tagcgaagaa gaaccacaga gccaccgccc 3180
 agctcccaga agtggggcca ctaagaagcc accgttggcc cagaaaccca gcatagcccc 3240
 caggacagac aaccagctgc acaaaaagga ttgtgtctac ccagctcaac ctgtgaacta 3300
 ctaggccctc aaggtgttca gcaggatggc ttgtgttgtt gcctgggctc catgtggactg 3360
 tctggcagtg gtaaaagggc cctcgagaag cctccaactc ctgcccgaag ggcctagtct 3420
 gtggagcagt tcatctggat gtgaattcat ttattttaa taggaactgc ctgcagcagc 3480
 tgggaccagc caggcctgag ccaacaaatc gcagcggaca tcagagatag tctgaatgct 3540
 gcgaggtatt tctttcttgc taagtttagt gacacactg ggaaaaggtc acataagcca 3600
 ggagcctctc ttgtcttgga ctcaaaagtc tgaggcctta agtgaacaac agaaagaggg 3660
 tccctgctgg ctaccagga taaggggatg accgtgacc cttgacga ggagagcagg 3720
 taagctgggt ggtgtctatca cctgggggccc ttgtgtctagg gcatccatgc tgggagcccc 3780
 aggaagcag ctacttgttg ggaagcctgg atcatctgag cctggggcag cctgtctcag 3840
 gtgtgtctc tgcctgtgac ctgaagcca cctcccacc ctacagtttt ccatctctct 3900
 ggcctactagt gtgtgtgttc attgcctacc ttgatgagta gatttcagcc ctctaaagc 3960
 tggggccttt cctctgtgct

<210> 11
 <211> 1068
 <212> PRT
 <213> Mouse

<400> 11
 Met Asn Ser Ile Lys Asn Val Pro Ala Arg Val Leu Ser Arg Arg Pro
 1 5 10 15
 Gly His Ser Leu Glu Ala Glu Arg Glu Gln Phe Asp Lys Thr Gln Ala
 20 25 30
 Ile Ser Ile Ser Lys Ala Ile Asn Ser Gln Glu Ala Pro Val Lys Glu
 35 40 45
 Lys His Ala Arg Arg Ile Ile Leu Gly Thr His His Glu Lys Gly Ala
 50 55 60
 Phe Thr Phe Trp Ser Tyr Ala Ile Gly Leu Pro Leu Ser Ser Ser Ser
 65 70 75 80

Ile Leu Ser Trp Lys Phe Cys His Val Leu His Lys Val Leu Arg Asp
 85 90 95
 Gly His Pro Asn Val Leu His Asp Tyr Gln Arg Tyr Arg Ser Asn Ile
 100 105 110
 Arg Glu Ile Gly Asp Leu Trp Gly His Leu Arg Asp Gln Tyr Gly His
 115 120 125
 Leu Val Asn Ile Tyr Thr Lys Leu Leu Thr Lys Ile Ser Phe His
 130 135 140
 Leu Lys His Pro Gln Phe Pro Ala Gly Leu Glu Val Thr Asp Glu Val
 145 150 155
 Leu Glu Lys Ala Ala Gly Thr Asp Val Asn Asn Ile Phe Gln Leu Thr
 165 170 175
 Val Glu Met Phe Asp Tyr Met Asp Cys Glu Leu Lys Leu Ser Glu Ser
 180 185 190
 Val Phe Arg Gln Leu Asn Thr Ala Ile Ala Val Ser Gln Met Ser Ser
 195 200 205
 Gly Gln Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Gln Asp Cys Ser
 210 215 220
 His Leu Tyr His Tyr Thr Val Lys Leu Met Phe Lys Leu His Ser Cys
 225 230 240
 Leu Pro Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe His Glu Gln
 245 250 255
 Phe His Ser Leu Lys Asn Phe Phe Arg Arg Ala Ser Asp Met Leu Tyr
 260 265 270
 Phe Lys Arg Leu Ile Gln Ile Pro Arg Leu Pro Glu Gly Pro Pro Asn
 275 280 285
 Phe Leu Arg Ala Ser Ala Leu Ala Glu His Ile Lys Pro Val Val Val
 290 295 300
 Ile Pro Glu Glu Ala Pro Glu Glu Glu Glu Pro Glu Asn Leu Ile Glu
 305 310 315 320
 Ile Ser Ser Ala Pro Pro Ala Gly Glu Glu Pro Val Val Val Ala Asp Leu
 325 330 335
 Phe Asp Gln Thr Phe Gly Pro Pro Asn Gly Ser Met Lys Asp Asp Arg
 340 345 350
 Asp Leu Gln Ile Glu Asn Leu Lys Arg Glu Val Glu Thr Leu Arg Ala
 355 360 365
 Glu Leu Glu Lys Ile Lys Met Glu Ala Gln Arg Tyr Ile Ser Gln Leu
 370 375 380
 Lys Gly Gln Val Asn Gly Leu Glu Ala Glu Leu Glu Gln Arg Lys
 385 390 400
 Gln Lys Gln Lys Ala Leu Val Asp Asn Glu Gln Leu Arg His Glu Leu
 405 410 415
 Ala Gln Leu Lys Ala Leu Gln Leu Glu Gly Ala Arg Asn Gln Gly Leu
 420 425 430
 Arg Glu Glu Ala Glu Arg Lys Ala Ser Ala Thr Glu Ala Arg Tyr Ser
 435 440 445
 Lys Leu Lys Glu Lys His Ser Ser Glu Leu Ile Asn Thr His Ala Glu Leu
 450 455 460
 Leu Arg Lys Asn Ala Asp Thr Ala Lys Gln Leu Thr Val Thr Gln Gln
 465 470 475 480
 Ser Gln Glu Glu Val Ala Arg Val Lys Glu Gln Leu Ala Phe Gln Met
 485 490 495
 Glu Gln Ala Lys Arg Glu Ser Glu Met Lys Met Glu Glu Gln Ser Asp
 500 505 510
 Gln Leu Glu Lys Leu Lys Arg Glu Leu Ala Ala Arg Ala Gly Glu Leu
 515 520 525
 Ala Arg Ala Gln Glu Ala Leu Ser Arg Thr Glu Gln Ser Gly Ser Glu
 530 535 540
 Leu Ser Ser Arg Leu Asp Thr Leu Asn Ala Glu Lys Glu Ala Leu Ser
 545 550 555 560
 Gly Val Val Arg Gln Arg Glu Ala Glu Leu Leu Ala Ala Gln Ser Leu
 565 570 575

Val Arg Glu Lys Glu Glu Ala Leu Ser Gln Glu Gln Gln Arg Ser Ser
 580 585 590
 Gln Glu Lys Gly Glu Leu Arg Gly Gln Leu Ala Glu Lys Glu Ser Gln
 595 600 605
 Glu Gln Gly Leu Arg Gln Lys Leu Leu Asp Glu Gln Leu Ala Val Leu
 610 615 620
 Arg Ser Ala Ala Ala Glu Ala Glu Ala Ile Leu Gln Asp Ala Val Ser
 625 630 635
 Lys Leu Asp Asp Pro Leu His Leu Arg Cys Thr Ser Ser Pro Asp Tyr
 645 650 655
 Leu Val Ser Arg Ala Gln Ala Ala Leu Asp Ser Val Ser Gly Leu Glu
 660 665 670
 Gln Gly His Thr Gln Tyr Leu Ala Ser Ser Glu Asp Ala Ser Ala Leu
 675 680 685
 Val Ala Ala Leu Thr Arg Phe Ser His Leu Ala Ala Asp Thr Ile Val
 690 695 700
 Asn Gly Ala Ala Thr Ser His Leu Ala Pro Thr Asp Pro Ala Asp Arg
 705 710 715
 Leu Met Asp Thr Cys Arg Glu Cys Gly Ala Arg Ala Leu Glu Leu Val
 725 730 735
 Gly Gln Leu Gln Asp Gln Thr Val Leu Arg Arg Ala Gln Pro Ser Leu
 740 745 750
 Met Arg Ala Pro Leu Gln Gly Ile Leu Gln Leu Gly Gln Asp Leu Lys
 755 760 765
 Pro Lys Ser Leu Asp Val Arg Gln Glu Glu Leu Gly Ala Met Val Asp
 770 775 780
 Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu Asp Ala Val Arg Arg
 785 790 795
 Ile Glu Asp Met Met Ser Gln Ala Arg His Glu Ser Ser Gly Val Lys
 805 810 815
 Leu Glu Val Asn Glu Arg Ile Leu Asn Ser Cys Thr Asp Leu Met Lys
 820 825 830
 Ala Ile Arg Leu Leu Val Met Thr Ser Thr Ser Leu Gln Lys Glu Ile
 835 840 845
 Val Glu Ser Gly Arg Gly Ala Ala Thr Gln Gln Glu Phe Tyr Ala Lys
 850 855 860
 Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala Ser Lys Ala Val Gly
 865 870 875
 Trp Gly Ala Thr Gln Leu Val Glu Ser Ala Asp Lys Val Val Leu His
 885 890 895
 Met Gly Lys Tyr Glu Glu Leu Ile Val Cys Ser His Glu Ile Ala Ala
 900 905 910
 Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val Lys Ala Asn Lys Asn
 915 920 925
 Ser Pro His Leu Ser Arg Leu Gln Glu Cys Ser Arg Thr Val Asn Glu
 930 935 940
 Arg Ala Ala Asn Val Val Ala Ser Thr Lys Ser Gly Gln Glu Gln Ile
 945 950 955
 Glu Asp Arg Asp Thr Met Asp Phe Ser Gly Leu Ser Leu Ile Lys Leu
 965 970 975
 Lys Lys Gln Glu Met Glu Thr Gln Val Arg Val Leu Glu Leu Glu Lys
 980 985 990
 Thr Leu Glu Ala Glu Arg Val Arg Leu Gly Glu Leu Arg Lys Gln His
 995 1000 1005
 Tyr Val Leu Ala Gly Gly Met Gly Thr Pro Ser Glu Glu Glu Pro Ser
 1010 1015 1020
 Arg Pro Ser Pro Ala Pro Arg Ser Gly Ala Thr Lys Lys Pro Pro Leu
 1025 1030 1035
 Ala Gln Lys Pro Ser Ile Ala Pro Arg Thr Asp Asn Gln Leu Asp Lys
 1045 1050 1055
 Lys Asp Gly Val Tyr Pro Ala Gln Leu Val Asn Tyr
 1060 1065

<210> 12
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sequencing primer

 <400> 12
 gaagataccc caccaaac 18

 <210> 13
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> cDNA primer

 <400> 13
 gcttgacagt gtatgcataa aggtggctgc agtcc 35

 <210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 14
 ggacatgtcc agggagtga atac 24

 <210> 15
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 15
 cuacuacuac uacuaggcca cgcgtcgact agtacggggg ggggg 45

 <210> 16
 <211> 516
 <212> DNA
 <213> Human

 <400> 16
 tctgtggaag gtttgaggag gagagaggag cagctggatg ctcttgggccc acggtcgccc 60
 ctgacatctcg cgcctctctcc tcctgctccg ggagaaataa tgtttccctg ggggatgaaa 120
 gcattctcttt gtgcgggctt taattgccat gttgttgctc caaggaggatg agtgccggcg 180
 ggaccagcag ctgggcacag ccaatgccag cagatggctg ccactccctc aggacgccca 240
 gccagctggc tcttgggagc gctgcccacc tctgcccaca gctgggcgccc tgcaaggaaac 300
 gccaccaccg tggggctggg ggaggttggc tggaggagga gaaagggggc ggctctggga 360
 gggctctcagc cactctcaga ggcttattea tctcatcctc ctttccctcc cccttcttgt 420
 ttttcagact gtcagcatca ataaggccat taatacgcag gaagtggctg taaaggaaaa 480
 acacgccaga aatatccctt ggatgttgct tgggaag 516

 <210> 17

<211> 193
 <212> DNA
 <213> Human

 <400> 17
 tgtttttccat aacccccccct caccgtgcat actgggcacc caccatgaga aaggggcaca 50
 gacctctcgg tctgtgtgca accgcctgcc tctgtctagg aaccacagtc cctgctggaa 120
 gttctgcat gtgttcacaa aactcctccg agatggacac ccgaacgtga gttcctgggg 180
 ctatgggggtg gca 193

 <210> 18
 <211> 104
 <212> DNA
 <213> Human

 <400> 18
 agtttctttt gccctgagc gtctgaagg actctctgag atacagaaat gaattgagtg 60
 acatgagcag gatgtgggtg agtttggaga tgtactcagg agcc 104

 <210> 19
 <211> 327
 <212> DNA
 <213> Human

 <400> 19
 aattcctggc tgcagatctc ttgactgtta tgttcttgtt gttgactctg ttcccccctcc 60
 tcttctctaaa agggccacct gagcgagggg tatggccagc tgtgcagcat ctacctgaaa 120
 ctgtctaagaa ccaagatgga gtaccacacc aaagtgaagc tctgcggaca gttctgcgcc 180
 caccgcgcgc tcccctgctc catcccttca gccctcctcc gggctcattt gtcagctctt 240
 tcaggtaata gacagccagc gcttctgagg aagtgtgcac atcatgtacc caagctgtga 300
 gagaggaag ccaccgccag gccccagc 327

 <210> 20
 <211> 331
 <212> DNA
 <213> Human

 <400> 20
 gggctcaagc aatcctccca cctcggcctc ccaagtagct gggaccacag gcgtgtgcca 60
 ceacgccggg ctgagagagg gctcttcatt tcttctgcc tgaactcctt cctctgcctc 120
 cctctcagaa tcccaggctc ccaggcaacc tgcagatgag tgaccgccag ctggacgagg 180
 ctggagaag tgagtggaac aacttgttaag tggctctctg cctgagccca gggaggagga 240
 agactctttt gaatcgtgac acttctcata agggtcatgg agggcctgat gggggggaggc 300
 cgtggctggg atggggacca aagccctgg g 331

 <210> 21
 <211> 470
 <212> DNA
 <213> Human

 <400> 21
 actgtcgctg tcaactgtga ctaccacagg ctgcatggcc ataataccca caaggctaag 60
 acttgagagc ggagtgtgtg gtgtgtttgc gcatgcacat gacatttga gactggagta 120
 gcgtgagcgc tgggggaggg gacaggtaac agaccggcct caggctgtgg agtgtaagct 180
 ctcttctctc ttgggtccag ttccagatta acagtggaga tgtttgacta cctggagtggt 240
 gaactcaacc ttttccaaac aggtgagtct ctccctccc gtctaaccga ggctctcatg 300
 ggaactacct aattcctagt cctcctctcc ctgcaaaagt tgacagcaca ggggtaggaa 360
 aatggagaca ttacacccc atctctggtc tctccaaacc cgtgacagg agggactgaa 420
 cctctcagc atttttcttt ttaagagaca aggtctcggc cgggtgcagt 470

 <210> 22
 <211> 565

<212> DNA
<213> Human

<400> 22
tcttcacctg ttttaatggg atactgttac ctatctcatg ggagtgtgt gaagggttaa 60
tgaattagat gaggttaaagc acgcacagaa tcggttccttg gtgtatgttg gacccctgcc 120
tcctgcccctc tgaagaggct gccctgtaatc cccctggcctc accacccttc tcctctacttc 180
ttattctcta gatttcaact cccctggacat gtctctcttg ggtctcttga cggcagcagg 240
cgactgcgcg ctgcgcgcgc tgatccagggt catctctggac tgcagccacc ttatgacta 300
cactgtcaag ctctctcttca aactccactc ctgtgagtac cgcgggcca atctctctac 360
atgagattca ggcagagggg aggatccag ctgtgagtag tccccagaga aacgcagtc 420
ttctcagtcg ctttggtctgt ctgctctctg tccaaaaggc cccggagctt ctgaccattg 480
tgaggataaa agagcagggc ccaggccttg gtgaccccg taaagccctt ggcttgccac 540
tcttgctgcc agtgtttacag gatct 565

<210> 23
<211> 233
<212> DNA
<213> Human

<400> 23
gggacagctc taggccagtc gtggcccttg cgactgtctg ccacatgcc cagggtagct 60
gggcccctcc cctctgagag ccccgctgtg gcttcctctc cctctggtcc cctccctctc 120
tcacactctt tccaatttct tccaggcctc ccagctgaca cctctgaagg ccaccgggac 180
cgctctatgg agcagctttac aaagttaagt gtccaagtaa caggaaatgga ggt 233

<210> 24
<211> 578
<212> DNA
<213> Human

<400> 24
tgaatccagc caccatggag tttatctcct tgacagcctg tgcctttggg ctggggaggg 60
ggcaggaagc ccagctggct gctctgtccc ctacatgggg ctgatgaaga caccacagcac 120
cctcagctc ctctccacc cctaggttga aagatctgt ctaccgtctc agaaccctgc 180
agtactcaaa ggcgtcatt cagatccccc agctgctctga ggttaagcatg cccaaccaca 240
cacccctggc actgcagagg ccccaggtac tctcttaagg gccggcgagg cctggccaagc 300
aagcactatt tgaggatgtg tctccgtctt cagaacccac ccaactctct cggagcctca 360
gccctgtcag aacatattcag cctctgtgtg gtgatccctg cagaggcctc atccccgcac 420
agcgcagcag tctatagaaa ggatgacctc atggagcctg atgcctctca gcaggtgagg 480
accacttggt agagaaaactt ggcctttctc ctacactgca agtacagggg agaggtctgg 540
ggagaccctg gccaaagccc attgactcta accaggtt 578

<210> 25
<211> 390
<212> DNA
<213> Human

<400> 25
aaaaaaattt aaaaaattaa acaggtctga accgtttaat tcgagaaagg gggcattctc 60
ccatataact caactgaccc acacacagaa ttctctggct ctctgactta ttctcactcc 120
tttttggtag accacagaat ttatttgaca acaagtctga tgacatctt ggcagttcat 180
tcagagtgta tcccttcaat ttcaacagtc aaaatggtt gaacaaggtt gagaagtgag 240
tccaagctgg gtccaagcag atggttcagg agctaaagtt agccatggtc tgccctaaaa 300
cactaaccaa agaggaattc ttaattgata tggggctctt tagatacaga acatcttgaa 360
gggttggggg caatggctta tgcctgtaat 390

<210> 26
<211> 547
<212> DNA
<213> Human

<400> 26
 aaaatcaata accatggatt tatgagtatt agattagtat ctggtaacat ttagagatata 60
 atttatggca ttctcaagaa ttgtcccaaa attaatacca gcttttaatt tctcccccctg 120
 agctcacaaat taaaaacaga gggatagaag cactatgaaa gcaaacctat tccccctctc 180
 ttcccaggga ccaacttaatt gagcgactat acagagagat cagtgagatt aaggcacagc 240
 tagaacaacat gaagactgag gtataacttg gatctgctct gcctttgcgc ttacacaaaa 300
 cacgtagatc ttgaatgcta aatttgcctc acactagcca ggcacagctgg ctcacacctg 360
 taatcttagc actttgggag gccaaaggag gaggaatacc tgaggtcggg agttggagac 420
 cagcctgggc aacaggggtga aacccccgtc tcaataaaa atgcaataat tagccgggtg 480
 tgttggcagg caccgtgtaat ccagctact cgggaagctg aggcattgaga attgcttgaa 540
 ctggga 547

<210> 27
 <211> 436
 <212> DNA
 <213> Human

<400> 27
 cccccagcca ctctaaagag gaccacaatt ccccgcccat catcccctgt tattgttgtt 60
 gattgagggg ctcttaatga ccagatggtc caaccctctt gggacgtgga gatttgactt 120
 aggggaatca ggtatttact tggaaagcatg gtaggaccgc cttctccggc ccattgcccc 180
 gaccctgggc agtggggcgt tggcctcatg accggagtc cccacagag ccagcgggtt 240
 gtgctgcagc tgaagggcca cgtcagcgag ctgggaagcag atctggccga gcagcagcac 300
 ctgcggcagc aggcgggcga cgactgtgaa ttctctcgag cagaactgga cgagctcagg 360
 aggcagcggg aggcacccga gaaggtctag cggagcctgt ctgagataga aagttagcgg 420
 tgggtggggg cggggg 436

<210> 28
 <211> 469
 <212> DNA
 <213> Human

<400> 28
 gacttgagcc caaggaggtc aaggtctgag tgaacagtga ttgtgccact gcaccccagc 60
 ctgggtgaca gagcaagact gtctcaaaac aaacaagga ggacctcta gggacctgtg 120
 ctcatgtcaa ggaaggcaag ggtccctgct aggttagact cctcacctgt gtctttaca 180
 atacaggaaa agctcaagcc aatgaacagc gatatagcaa gctaaaggag aagtaacagc 240
 agctgtgtca gaaccaagct gacctgctg ggaaggttaag accctcagcc cctgtcacca 300
 tctctgagcc cctgcacctc tagggagaga gcggctcagg cctgtggctt ccccggggcc 360
 agcaaccctc acattgatct ctaaggcatt gcggtcatc cgggaaccac accttttcag 420
 gcttctctgc ctctgtgtct tgggtctgtt cctgggtgccc aatcccatg 469

<210> 29
 <211> 359
 <212> DNA
 <213> Human

<400> 29
 gggtaggaaa gtgattcctg tgtctgactc tagggcacgc acagcctgag tatgattgtc 60
 ctagaaggag gatgtctctt aagcctggga tctctgtgtt caagacactg ttcttttttt 120
 gcagaattgca gaggtgacca aacaggtgtc catggccaga caagcccagg tagattttga 180
 acgagagaaa aaagagctgg aggtattggt ggagcgcctc agtgaccagg gccagcggaa 240
 ggtgagtcgg acgaggagca ctggggaat gagggagggg gctgttgagt tgggtggcgg 300
 ggtttgtgg cctctgtctc catgggcagt tctgtgggtc ggttggtatc acacagacg 359

<210> 30
 <211> 209
 <212> DNA
 <213> Human

<400> 30
 gttgatcgct tgggacgttt ttacattttt atattctttg tcaatgtcac ccagatcaga 60

gtccctctgt	ttttctcttc	tttcagactc	aagaacagct	ggaagttcta	gagagcttga	120
agcaggaaact	tgccacaagc	caacgggaagc	ttcaggttct	gcaaggcagc	ctggaaactt	180
ctgccagggt	aaataacctc	ttttttttt				209

<210> 31
 <211> 485
 <212> DNA
 <213> Human

<400> 31						
ccccactgc	aatcagtggt	tccccgggag	ggaatcagag	tggcagggtta	aagagccatc	60
accttccag	tccttgcaac	ccggtggttg	gttggaacctc	tgggaagtag	ggactgttta	120
actcaaccag	cgtctccctc	tttctctgtg	gtcacctttg	cagtcagaag	caacttgggc	180
agccaggttc	gccgagctag	agaaggagcg	ggacagcctg	gtgagtggcg	cagctcatag	240
ggaggaggaa	ttatctgtct	ttcggaaaga	actgcaggac	actcagctca	aactggccag	300
cacagaggg	cacggacatg	gacacgagcg	agcaccctgt	aattcccacc	gagggcctct	360
gcgcattgc	ggaggctggg	aggaccccg	ggctgctgag	aaggggtttg	gggccttggc	420
ctgattgtgc	agacattctg	taggtgtaat	gccagcaggc	cctgcattgc	ctgcagagtc	480
catga						485

<210> 32
 <211> 468
 <212> DNA
 <213> Human

<400> 32						
ttaactggctt	ggacctcatt	ggccatgact	tgagctaaga	tgctaagagc	cccagccagg	60
tcatctgtct	caggtttcatt	atggagttcta	gggcagactc	tcacctccct	ggacctcttt	120
tagaatctat	gtgccagctt	gccaaagacc	aacgaaaaat	gcttctgtgt	gggtccaggaa	180
aggctgcggg	gcaggtgata	caagacgccc	tgaaccagct	tgaagaacct	ccctctcatca	240
gctgcgtctg	gtctgcaggt	acacttgcaa	ttgcggctct	ggcagggggc	aggtctttac	300
agcctgagac	ttctgtgatg	ttgaattcca	tgtgagactt	agctcagggg	ctctcagccc	360
agcagcatgt	cagcattacc	ttagggggcg	ccaggcccca	tcctagatca	gttaccatgt	420
gaaactctgt	gcattagtgc	ctatacacta	gtatttttagt	atttttctt		468

<210> 33
 <211> 393
 <212> DNA
 <213> Human

<400> 33						
cactagttaag	ctctctcatt	cagtgtctaa	ttaacgagga	tgaagccagc	tatgagaact	60
tgctctgacc	ttgcctctgt	ttccctctca	cagatcacct	ccctccacag	gtcacatcca	120
tttccagctg	ctcgcagcaa	ctggagaaaa	gctggagcca	gtatctgtggc	tgcccagaag	180
gtaagaaatg	ccaaggacag	tctctgtctg	ctagtgtatg	ccagacaggg	ttcagaagca	240
ctgtaaatcg	gggatagtga	caggtccctc	tgcatcaaga	aaggcatgta	ggcaactcat	300
acaagaagaag	catgtaggca	actcataaaa	cgggaggaga	gggtatgaaa	gtgtcaccat	360
caaccagacc	tgagaaacct	ctctttccaa	tcc			393

<210> 34
 <211> 421
 <212> DNA
 <213> Human

<400> 34						
ggcctgccca	gaaggttaaga	atggccaagg	acagttctctg	tcggctagtgt	atggccagac	60
aggggttcaga	agcacctgaa	tgccggggata	gtgacaggctc	ccctctgcatc	aagaaaggca	120
tgtagggcaac	tcatacaaga	aaggcatgta	ggcaactcat	aaaacgggag	gagagggtat	180
gaaagtgtca	ccatcaacca	gacctgagaa	actctctctt	ccaatcctgtg	cagacatcag	240
tggaactcttc	cattccataa	ccctgctggc	ccacttgacc	agcgacgcca	ttgctcatgt	300
tgccaccacc	tgctctcagag	ccccacctga	gcctgcccag	tgtgagtact	ggggcatgag	360
gggctgtcca	tggaagcagg	gagcaggggg	gctctaaaaa	tctctgttgg	gcccggcgca	420

g		421
<210>	35	
<211>	498	
<212>	DNA	
<213>	Human	
<400>	35	
aggccgagggc	aggagaatcg	cttgaactca
cgccactgca	ctccagccctg	ggcaacaaga
attgccttgt	atctccagca	ctgaccgagg
ctcactctggc	ctccctcgag	gaagaggga
ggaactgcct	gagcaagatc	aaggccatcg
gcattgttat	tcttctgggt	gtgcgtgctg
agctagtctt	tctcgactt	agaacttgat
ctggccgggt	gcagtgtatt	atgcgtgtaa
gatcacttga	ggctagac	tcccgacct
		ttggggagcc
		gagtcaggag
		60
		120
		180
		240
		300
		360
		420
		480
		498
<210>	36	
<211>	427	
<212>	DNA	
<213>	Human	
<400>	36	
ccctgtggct	tgacagaagt	gtttgctggg
tacagatggc	agaggagaag	agacaggagg
ttcaacagg	ctctcgcca	ggggactgga
ggacaaggag	atggcgccca	cttcagctgc
aggagggttc	tgacagatct	ccctgaacga
ctcatataac	atgtcacagt	cgcttcattaa
gaatttgcca	ggcacagtgg	ctcatgcctg
gtccagg		taaccccgac
		accttggggag
		gatcacttga
		60
		120
		180
		240
		300
		360
		420
		480
		497
<210>	37	
<211>	367	
<212>	DNA	
<213>	Human	
<400>	37	
ccccctgaat	agggttagagt	ctggattcct
cttggggagct	tccagattca	ggtttccag
taagacatta	gtggatcctt	aattattcaag
aggagatgct	cagcaaatcc	cgagcaggag
ggtcggctctg	agcggcattg	tgaggacttag
ctataactttg	catacttatt	aggggaattag
tgagtctg		aggagagcag
		tagcagccac
		gggggaagggc
		60
		120
		180
		240
		300
		360
		367
<210>	38	
<211>	502	
<212>	DNA	
<213>	Human	
<400>	38	
cccccgagaa	tgttccagca	acctcagcac
gtccctttggc	taggagtggtg	gaagagaacc
cagtgatacc	tcgacttgggt	tgtttggcag
agctattcag	gtgctcatcg	tggcctctaa
cagggtgagc	gtgggtgtgg	gccctgggca
ctccaaaggga	ctctgtgatg	ctgcgctctt
ccactcctgt	agatatcagc	agaggccctg
aggggtggcc	aggcatgtgt	cccaactcca
acttgctctg	ggagcccttt	ctt
		ctctcttacc
		gtcgtgttca
		gtacttgggt
		ggaagaggag
		gcactgggtga
		tcacacttag
		gggagaagtc
		gctccctctg
		cacaggcaga
		catgtgtgga
		60
		120
		180
		240
		300
		360
		420
		480
		502

<210> 39
 <211> 437
 <212> DNA
 <213> Human

 <400> 39
 ttttggctct tgaattctct tcttttttgt aaaatgggaa tactaatgct tatgtctcag 60
 agttactatg aggatgattt gggataatat atgtataaaa gcacctgccca tatagtacat 120
 gctcaataaa aggtggctat tactattttt tatttcoccta gggtagacga tcccctaaga 180
 agttttatgc caagaaactct cgaatggacag aaggacttat ctgagcctcc aaggctgtgg 240
 gctggggagc cactgtcatg gtgtgaagtat ctattgtgtac caagggtcct cccatgaccc 300
 ctcttccatt gatccactcc aaacaatagc taaggaggga aaaaaaaatc tgtcccttag 360
 aaataaacta ttgatccagg agtcaatagg accgagttaa caaggggagcc tggctctccc 420
 aggggacaca gggcagg 437

 <210> 40
 <211> 351
 <212> DNA
 <213> Human

 <400> 40
 gggagcctcg ctctcccagg ggacacaggg caggagcctt ccctccctg tttagccaag 60
 ggcgatgggg tggctctgag gtgggattgt gaggaggttg cagctcattt gcccgtaacc 120
 tagtccctct tgcgtttttc catcaaggat gcagctgacc tgggtgtaca aggcagaggg 180
 aaatttgagg agctaattgt gtgtctctat gaaattgtct ctgagacagc ccagcttgtg 240
 gctgcattca aggtaggacc ttgctggacc tcttagagc ctggaagcc tgggttagaga 300
 gtactaggct aggttaaaga gtacttggtt gcgttaggca gtacttggtt g 351

 <210> 41
 <211> 418
 <212> DNA
 <213> Human

 <400> 41
 cttttttatat gatagatatg tcaggagctg actatagtca gcagattttg agaagctgat 60
 tgggtgattgc cgtttggccc acatatgttt gctaagaacc atcagagcaa ttactgtatt 120
 cagtccttgt tgctctaggt gttgtatgaa cctaactctg ctttgtcttg gttagtgaaa 180
 gctgataagg acagcccaaa cctagcccag ctgcagcagg cctctcgggg agtgaaccag 240
 gccactggcg gcgttgtggc ctcaaccatt tccggcaaat cacagatcga agagacaggt 300
 agcctttcca aagggacccct tttttaccct accctgttga gctcttctct gcatccttcc 360
 cgttgatccc aaacaaatcc cacaggactg tgtctaaatt ctttcatatt tttcatct 418

 <210> 42
 <211> 279
 <212> DNA
 <213> Human

 <400> 42
 tttccacaga gcattggcat tggctgcctc tcagggtgcca gtcagccagg gtagaatttg 60
 atgagaccct cttgtttcca tcttgcgaga caacatggac tcttcaagca tgacgctgac 120
 acagatcaaa cgtcaaaagc tgggagagct tggtaggggt ctgagagtag aaaaatgaat 180
 gcagaaggag cgtcaaaagc tgggagagct tggtaggggt cactacgagc ttgctgggtgt 240
 tgctgagggc tgggaagaag gtaagctgac tcaaaaggat 279

 <210> 43
 <211> 3715
 <212> DNA
 <213> Human

 <400> 43
 aacataaatt atcattgtct tttaggaaca gaggcatctc cacctacact gcaagaagtg 60

gtaaccgaaa aagaatagag ccaaaccaac accccatagt tcagtgtaaa tccttgttac 120
 ctatctcgtg tgtgttattt cccagccac aggcacaaatc ctggagtc caggggcagc 180
 ccacaccagt ccattaccaca gtgcggagga catgcatgac acttcccaaa gactccctcc 240
 atagcagacat gctttctgtt tggaccatgt gtcattctctg ttcttttccc gctctccctg 300
 tttagctcca ggctggccag tgctgccccat gacgaagcct aggtacgaag aggggtgtgt 360
 gggggcaggg ccactcaaca gagaggacca acatcccaag ctgctgacta ttgtgccccc 420
 acaaccaatgg gtatccttaa tagaggagct gcttgttgtt ggttgacagc ttggaaaaggg 480
 aagatcttat gctcttctgt ttctgttttc ttccagttc atcattgtca 540
 caactctgtg agcatcacag ggctgatgga ttccaaaacca ggaactaacc ttgagatctg 600
 cacagtcaag aggacggccag gagtgtcctg gctgtgaagt ccaaagccat tctccccctc 660
 tttgggcagt gccatgatt tccaactgct ctatgggtgt ttggttgggt ttttgggttt 720
 tttttttttt ttttaagttt cactcacata gccaaactct ccaaagggca caccctctgg 780
 gctgagtcct caggggcccc caactgtggt agctccagcg atggtgctg ccagcctctc 840
 cgggtgctcca tctccgctcc cacactgacc aagtgtctgg ccaaccagtc catgtccagc 900
 ggtcaggcgg agctcgtgag tgacagcttt cctcaaaaag cagaaggaga gtagtgctc 960
 ttccctctta gggcgtgaat ccggcgggaaa gctctgtccc gctcttcaaa ggggaagagc 1020
 aacagaaaga ggttcacaga ggttcacaca gccagctccc cgtgcagagg ctcaaaaact 1080
 tgatcacatg cttgaatgga gctggtgaga tcaacaacac tacttcccgt ccggaatgaa 1140
 ctgtccgtga atgttctctg tcaaggcgcc cgtctccctt ggcacagaga cggagtgtgg 1200
 gagtgtattc accactcttt ctgcagacgt ctgcttggc atcctctga ataggaagt 1260
 cgttccactt tctacgcaat tgacaaaccc ggaagatcag atgcaattgt tcccatcagc 1320
 gaagaacccct atacttgggt tgcctaccct agtattttt actaacctcc cttaagcagc 1380
 aacagcctac aacagagatgc ttggagcaat cagaacttca ggtgtgactc tgcaaaagct 1440
 catctttctg cccgctctaca tcaagcttca tcatttggag ctcttgggtc agagaaaaatg 1500
 gttactgact tggatcccaa agcaaggaga tcatttggag ctcttgggtc agagaaaaatg 1560
 agaaagaga gaggcagcgg ctccaaactc ttccagcac atgcgcagag ctcttctgctg 1620
 cttctggaga ggaatgagca agagggcaca tgaacagctt gccagagatg gcagcccaa 1680
 cagcactttt cctcttctag atggaccoca gcatttaagt gacctctga tcttgggaaa 1740
 acagcgtctt cctcttctat ctatagcaac tcatttgggt tagccatcca gacttccca 1800
 ggatctgtct caacagaata ttgctaggtt ttgtcacatg accgggttctg agacttctgt 1860
 ttgatcactg tgaaccaaacc cccatctccc tagcccaccc cctccctcca ctctctctg 1920
 gtgcattttc taagtgggac attcaaaaaa ctctctccca ggaactcgga tgacactact 1980
 cagacgtgtg acctccatac ttgggttaagg aagtatcagc actagaattt gggcagctct 2040
 aatgttgaat gctgctttct gcttagtatt tttttgattc aaggctcaga aggaatgggt 2100
 cgtggctcc ctgtcccaact tgtggcaact gttgttcttt gatgggggtc 2160
 aacatttcca aaagtgtcta gtctcactt ctgadtctca gccattctaa ctcattgtt 2220
 cccaattacc aagggtgtgc cgggcacagt ggtccacgcc tgtaatccca gcaactttag 2280
 aggtcgtggt gctaggatca cctgaggcca ggagtcaaag accagcctgt ccaactaggt 2340
 gaaaccccca tctctactaa aaataccaaa aattagccga cggtatgac ggggtccctg 2400
 aatccacgtc actcaggagc ctgagacagg agaatacctt gaacccaga gccagaggtt 2460
 cgagtgagct gagatcaagc cattgtactc cagcctgggc aacaagagca aactctcgt 2520
 tcaaaaaaaa aaaaaaatta caaatggggc aaacagtcta gtgtaatgga tcaaatlaag 2580
 attcttggcc cagcggggca cagtggcgca tgctgtaat ccagaaactt tggggaggca 2640
 agacggagtg atgtctttag ctgaggaggt ttgagacagg ctgggcatac tagcagagc 2700
 tcatctctac taaaattcaa aaacaaaatt ttggtgtgat gatgtgtgat cctctagctc 2760
 tcaagtattt ggggagctaa ggtgggagaa ttgcttgagc ttgggaagtc gaggctgacg 2820
 tcagccctga cgaactccgc ctgggtgaca gagttagacc cgtgctcaaa 2880
 aaaaaaaaga tctctgttca gagccagccc caggagttgt aggtctaat gagccatgat 2940
 tctccactgc actccagcct gagttagaca gcgagactcc atctctttaa aaacaaaaca 3000
 aaaaattatc gaatgactct gtctctaaaa agaagccaca gaaatgttta aaaaactcat 3060
 cgaattagcc tgactataa cggttaaaga gcactttaa cagaagcaga ggctaatca 3120
 ggttcacatg aggaagttag ttgtcagatgt cacataata ctcttctaat agctcaagat 3180
 agaatgtcta tagacaaat ctgactgttc atctgttctc ttcttcaaaa 3240
 tgaagtgaag gactatttta atgacacacc ttggttata acgggaata catctatag 3300
 ctcaaaatga acctgcaagc ctcttaaatg agtcaactag catcaactag tcaagacttc 3360
 gggtagcgct aaataggtca tgacaagatg ggcacagcag aaaaatcag cttaagatgc 3420
 caagaagttt aaaaaaacg tgcattgttt acttaagttt gtaagacagt gccctgagac 3480
 ctcttagaaa aagatgtttt ttacataag agaaagaagg ccagacatgt gtctctagc 3540
 gtttaactccc agcacttttg gaggcagggg cgggtggatc acctgaggtc aggaggtcaa 3600
 gactagcgtg gccacaatg tgaaaacccc ttctactaaa aaatacaaaa attagccgtc 3660
 catggttgca ggcgcctata atccacagcta ctggggaggg tcaggcagga gaatc 3715